IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s): Sanders	
Application No.: 10/537,280	Group Art Unit:
Filed: 5/27/2005	Examiner:
Title: Binding Partners for the Thyrotropin Receptor and Uses Thereof	
Attorney Docket No.: URQU.P-016	

Assistant Commissioner for Patents
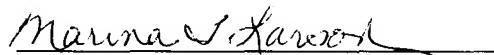
P.O. Box 1450

Alexandria, VA 22313

Response to Notification to Comply

Dear Sir:

Responsive to the Notification to Comply mailed November 9, 2005 for the above-captioned application, Applicants have electronically filed a sequence listing for this application. A printed copy of the sequence listing is attached. The undersigned certifies that the printed copy and the electronic copy have the same content. No new matter has been added.

The notification also indicated an additional claim fee of $400. A credit card authorization to pay this fee is included with this submission.

Respectfully submitted,

Marina T. Larson, Ph.D
Attorney/Agent for Applicant(s)
Reg. No. 32038

(970) 468 6600

SEQUENCE LISTING

<110>   Sanders, Jane
        Furmaniak, Jadwiga
        Smith, Bernard Rees

<120>   Binding Partners for the Thyrotropin Receptor and uses thereof

<130>   URQU.P-016

<140>   US 10/537,260
<141>   2003-11-28

<150>   PCT/GB2003/005171
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<150>   GB 0227964.4
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            35   40   45

Gly Arg Ile Asp Pro Thr Asp Ser Tyr Thr Asn Tyr Ser Pro Ser Phe
    50   55   60

Lys Gly His Val Thr Val Ser Ala Asp Lys Ser Ile Asn Thr Ala Tyr
65   70   75   80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Gly Met Tyr Tyr Cys
                85   90   95

Ala Arg Leu Glu Pro Gly Tyr Ser Ser Thr Trp Ser Val Asn Trp Gly
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Gln Gly Thr Leu Val Thr Val Ser Ser
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Ser Leu Lys Ile Ser Cys Arg Gly Ser Gly Tyr Arg Phe Thr Ser Tyr
         20   25   30

Trp Ile Asn Trp Val Arg Gln Leu Pro Gly Lys Gly Leu Glu Trp Met
         35   40   45

Gly Arg Ile Asp Pro Thr Asp Ser Tyr Thr Asn Tyr Ser Pro Ser Phe
    50   55   60

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Lys Gly His Val Thr Val Ser Ala Asp Lys Ser Ile Asn Thr Ala Tyr
65                  70                  75                  80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Gly Met Tyr Tyr Cys
                85                  90                  95

Ala Arg Leu Glu Pro Gly Tyr Ser Ser Thr Trp Ser Val Asn Trp Gly
            100                 105                 110

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Ala Val Asn Trp Tyr Gln Gln Leu Pro Gly Lys Ala Pro Lys Leu Leu
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Ile Tyr Tyr Asp Asp Gln Leu Pro Ser Gly Val Ser Asp Arg Phe Ser
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Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Arg Gly Leu Gln
65                  70                  75                  80

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agtccatcct tcaaaggcca cgtcaccgtc tcagctgaca agtccatcaa cactgcctac   240

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ccaggaaagg ctcccaaact cctcatttat tatgatgatc aactgccctc aggggtctct   180

gaccgattct ctggctccag gtctggcacc tccgcctccc tggccatccg tgggctccag   240

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Ser Val Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr
            20   25   30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Glu Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Asn Gln Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80

Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                85   90   95

Ser Arg Asn Tyr Gly Ser Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
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Thr Thr Leu Thr Val Ser Ser
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            20   25   30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Glu Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Asn Gln Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65   70   75   80

Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
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            35   40   45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
        50   55   60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Thr Glu
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                20   25   30

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            35   40   45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
        50   55   60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Thr Glu
65   70   75   80

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                85   90   95

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aatcaaaagt tcaagggcaa ggccacattg actgtagaca aatcctccag cacagcctac   240

atgcacctca gcagcctgac atctgaggac tctgcggtct attactgttc aagaaactac   300

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ttcagtggca gtgggtctgg gacctcttac tctctcacaa tcagcagcat ggagactgaa   240

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